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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=6; day=23; hr=8; min=41; sec=19; ms=406; ]

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Reviewer Comments:

#### SEQUENCE LISTING

<110> Max-Planck-Gesellschaft zur Förderung der Wissenschaften  
e.V.

Please remove the foreign accent marks in the above <110> response;  
foreign accent marks are non-ASCII characters which cannot be processed.

<120> Cell line comprising vector encoding truncated FLK-1 receptor  
Div. of US 09/766 678 (Pat. No. 6 872 699)

Please remove "Div. of US 09/766 678 (Pat. No. 6 872 699)" from the  
above <120> response; just show the invention title. Move all prior  
application data to the <150> and the <151> lines. See below:

<150> US 09/766,678

<151> 2001-01-23

The <150> is the prior application number; the <151> is the prior filing  
date.

<210> 1

<211> 5470

<212> DNA

<213> Unknown

<220>

<223> SEQ ID NO: 1

The above <223> response is an insufficient explanation of "<213>

Unknown": although the <213> response is "Unknown", please try to indicate the source of the genetic material. Same type of error in Sequences 2-11.

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Application No: 10799782 Version No: 2.0

Input Set:

Output Set:

Started: 2009-06-15 15:22:43.641  
Finished: 2009-06-15 15:22:45.942  
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 301 ms  
Total Warnings: 11  
Total Errors: 0  
No. of SeqIDs Defined: 11  
Actual SeqID Count: 11

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
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W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)

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<212> DNA  
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<220>  
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<222> (286)..(4386)

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tct gtg ggt ttg act ggc gat ttt ctc cat ccc ccc aag ctc agc aca 393  
Ser Val Gly Leu Thr Gly Asp Phe Leu His Pro Pro Lys Leu Ser Thr  
25 30 35  
  
cag aaa gac ata ctg aca att ttg gca aat aca acc ctt cag att act 441  
Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr Leu Gln Ile Thr  
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Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Ala Gln Arg  
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Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly Gly Gly Asp Ser  
70 75 80  
  
atc ttc tgc aaa aca ctc acc att ccc agg gtg gtt gga aat gat act 585  
Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val Gly Asn Asp Thr  
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Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile Ala Ser Thr Val  
105 110 115  
  
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Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val Ser  
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165 170 175 180	
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Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr Met Ile Ser Tyr	
185 190 195	
gcc gcc atg gtc ttc tgt gag gca aag atc aat gat gaa acc tat cag	921
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tct atc atg tac ata gtt gtg gtt gta gga tat agg att tat gat gtg	969
Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr Asp Val	
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230 235 240	
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Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Leu Asp Phe	
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Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys Lys Ile Val Asn	
265 270 275	
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Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys Met Phe Leu Ser	
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Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln Gly Glu Tyr Thr	
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Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn Arg Thr Phe Val	
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Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser Gly Met Lys Ser	
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Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val Ile Leu Thr Asn	
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455 460 465	
tcc tac aga ccc ggc caa aca agc ccg tat gct tgt aaa gaa tgg aga	1737
Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys Lys Glu Trp Arg	
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His Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu Val Thr Lys Asn	
485 490 495 500	
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Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val Ser Thr Leu Val	
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Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys Glu Ala Ile Asn	
520 525 530	
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Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His Val Ile Arg Gly	
535 540 545	
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Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr Glu Gln Glu Ser	
550 555 560	
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Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe Glu Asn Leu Thr	
565 570 575 580	
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Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile Val Ala Phe Gln	
615 620 625	
aat gcc tct ctg cag gac caa ggc gac tat gtt tgc tct gct caa gat	2217
Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys Ser Ala Gln Asp	
630 635 640	
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Lys Lys Thr Lys Lys Arg His Cys Leu Val Lys Gln Leu Ile Ile Leu	
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695 700 705	
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760 765 770	
gcc atg ttc ttc tgg ctc ctt ctt gtc att gtc cta cgg acc gtt aag	2649
Ala Met Phe Phe Trp Leu Leu Leu Val Ile Val Leu Arg Thr Val Lys	
775 780 785	
cgg gcc aat gaa ggg gaa ctg aag aca ggc tac ttg tct att gtc atg	2697
Arg Ala Asn Glu Gly Glu Leu Lys Thr Gly Tyr Leu Ser Ile Val Met	
790 795 800	
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Asp Pro Asp Glu Leu Pro Leu Asp Glu Arg Cys Glu Arg Leu Pro Tyr	

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cct ctt ggc cgc ggt gcc ttc ggc caa gtg att gag gca gac gct ttt				2841
Pro Leu Gly Arg Gly Ala Phe Gly Gln Val Ile Glu Ala Asp Ala Phe				
	840	845	850	
gga att gac aag aca gcg act tgc aaa aca gta gcc gtc aag atg ttg				2889
Gly Ile Asp Lys Thr Ala Thr Cys Lys Thr Val Ala Val Lys Met Leu				
	855	860	865	
aaa gaa gga gca aca cac agc gag cat cga gcc ctc atg tct gaa ctc				2937
Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu Met Ser Glu Leu				
	870	875	880	
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Lys Ile Leu Ile His Ile Gly His His Leu Asn Val Val Asn Leu Leu				
	885	890	900	
ggc gcc tgc acc aag ccg gga ggg cct ctc atg gtg att gtg gaa ttc				3033
Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val Ile Val Glu Phe				
	905	910	915	
tgc aag ttt gga aac cta tca act tac tta cgg ggc aag aga aat gaa				3081
Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Gly Lys Arg Asn Glu				
	920	925	930	
ttt gtt ccc tat aag agc aaa ggg gca cgc ttc cgc cag ggc aag gac				3129
Phe Val Pro Tyr Lys Ser Lys Gly Ala Arg Phe Arg Gln Gly Lys Asp				
	935	940	945	
tac gtt ggg gag ctc tcc gtg gat ctg aaa aga cgc ttg gac agc atc				3177
Tyr Val Gly Glu Leu Ser Val Asp Leu Lys Arg Arg Leu Asp Ser Ile				
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Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly Phe Val Glu Glu Lys Ser				
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	985	990	995	
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Tyr Val Arg Lys	Gly Asp Ala Arg Leu	Pro Leu Lys Trp Met Ala	
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Pro Met Ser Glu	Thr Leu Ser Met Glu	Glu Asp Ser Gly Leu Ser	
1180			